

#10

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/501,127A

Source: PT/10

Date Processed by STIC: 4/13/05

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PCT

RAW SEQUENCE LISTING

DATE: 04/13/2005

PATENT APPLICATION: US/10/501,127A

TIME: 16:09:48

Input Set : A:\Sequence 2002-032 US.txt

Output Set: N:\CRF4\04132005\J501127A.raw

3 <110> APPLICANT: ID-Lelystad, Instituut voor Dierhouderij en Diergezondheid.
 5 <120> TITLE OF INVENTION: Paramycobacterial diagnostics and vaccines
 7 <130> FILE REFERENCE: 2002-032-US
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/501,127A
 C--> 9 <141> CURRENT FILING DATE: 2004-07-09
 9 <160> NUMBER OF SEQ ID NOS: 22
 11 <170> SOFTWARE: PatentIn version 3.2
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1175
 15 <212> TYPE: DNA
 16 <213> ORGANISM: mycobacterium avium paratuberculosis
 19 <220> FEATURE:
 20 <221> NAME/KEY: CDS
 21 <222> LOCATION: (134)..(1144)
 23 <400> SEQUENCE: 1

24	aattgcctca cgattcaata tcaccactct agtaatagga ttcccactcg taccatcgac	60
26	tgtgtgtgat tcctgccaga cagcatcggc ggggcgcgcc gacacaacac atagtcagat	120
28	agaggagact tcc gtg ccg aac cga cgc cga cgc aag ctt tcg aca gcc	169
29	Val Pro Asn Arg Arg Arg Arg Lys Leu Ser Thr Ala	
30	1 5 10	
32	atg agc gcg gtc gcc gcc ctg gca gtg gcg agt cct tgc gca tac ttc	217
33	Met Ser Ala Val Ala Ala Leu Ala Val Ala Ser Pro Cys Ala Tyr Phe	
34	15 20 25	
36	ctt gtc tac gaa tcg acg gcc ggc aac aag gcg ccc gag cac cac gag	265
37	Leu Val Tyr Glu Ser Thr Ala Gly Asn Lys Ala Pro Glu His His Glu	
38	30 35 40	
40	ttc aag cag gcc gca gtg atg agc gat ctg ccg ggc gag ctg atg ggt	313
41	Phe Lys Gln Ala Ala Val Met Ser Asp Leu Pro Gly Glu Leu Met Gly	
42	45 50 55 60	
44	gcg ctg tcg cag ggc ctg tcg cag ttt ggg atc aac ctg ccc ccg gtg	361
45	Ala Leu Ser Gln Gly Leu Ser Gln Phe Gly Ile Asn Leu Pro Pro Val	
46	65 70 75	
48	ccc gcc ctg agc ggc ggc gcc acc agc act ccc ggt ctg gcc agc ccc	409
49	Pro Ala Leu Ser Gly Gly Ala Thr Ser Thr Pro Gly Leu Ala Ser Pro	
50	80 85 90	
52	ggc ctg ggt agc ccc ggc ctg ggc acg ccc ggc ctg gga acg ccg ggc	457
53	Gly Leu Gly Ser Pro Gly Leu Gly Thr Pro Gly Leu Gly Thr Pro Gly	
54	95 100 105	
56	ctg acc aat ccc ggt ctg acg agc ccc ggt gcg acc agt ccc ggc ctg	505
57	Leu Thr Asn Pro Gly Leu Thr Ser Pro Gly Ala Thr Ser Pro Gly Leu	
58	110 115 120	
60	acc agt ccc ggc ctg acc agt cct ggt ttg acc agc ccc ggt ctg acc	553
61	Thr Ser Pro Gly Leu Thr Ser Pro Gly Leu Thr Ser Pro Gly Leu Thr	

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62 125          130          135          140
64 agc ccg ggt gcg gcg ccg acg acg ccc ggg ctc acc gcg ccc ggc gcg      601
65 Ser Pro Gly Ala Ala Pro Thr Thr Pro Gly Leu Thr Ala Pro Gly Ala
66          145          150          155
68 ctg ccg acc acg ccg ggc ggc ggg gtc gcc acc ccc ggc gcc ggg ctc      649
69 Leu Pro Thr Thr Pro Gly Gly Gly Val Ala Thr Pro Gly Ala Gly Leu
70          160          165          170
72 aac ccc gcg ctg tcc aac ccc ggg ctg acc agc ccg gcc ggg acg gcg      697
73 Asn Pro Ala Leu Ser Asn Pro Gly Leu Thr Ser Pro Ala Gly Thr Ala
74          175          180          185
76 ccg ggg ctg ggc agc ccg acc gtg gcg ccg agt gag gtg ccg atc gac      745
77 Pro Gly Leu Gly Ser Pro Thr Val Ala Pro Ser Glu Val Pro Ile Asp
78          190          195          200
80 tcc ggg gcc ggc ctg gac ccg ggc gcc ggt ggc acc tac ccg atc ctg      793
81 Ser Gly Ala Gly Leu Asp Pro Gly Ala Gly Gly Thr Tyr Pro Ile Leu
82 205          210          215          220
84 ggc gac ccg tcg acc ttc ggt aac gcc tcg ccg atc ggc ggc ggt ggc      841
85 Gly Asp Pro Ser Thr Phe Gly Asn Ala Ser Pro Ile Gly Gly Gly Gly
86          225          230          235
88 acc ggt ctg ggc ggc ggc tcg agc tcg ggt ggc agc ggc ggc ctg gtc      889
89 Thr Gly Leu Gly Gly Gly Ser Ser Ser Gly Gly Ser Gly Gly Leu Val
90          240          245          250
92 aac gac gtg atg caa gcc gcc aac cag ctc ggc gcg ggt cag gcg atc      937
93 Asn Asp Val Met Gln Ala Ala Asn Gln Leu Gly Ala Gly Gln Ala Ile
94          255          260          265
96 gac ctg ctc aag ggc ctg gtg atg ccg gcg atc acg cag ggc atg cac      985
97 Asp Leu Leu Lys Gly Leu Val Met Pro Ala Ile Thr Gln Gly Met His
98          270          275          280
100 ggc ggc gcg gcc gcg ggt gct ttg ccc ggc gcg gcc ggt gct ctg ccc      1033
101 Gly Gly Ala Ala Ala Gly Ala Leu Pro Gly Ala Ala Gly Ala Leu Pro
102 285          290          295          300
104 ggc gcg gcc ggc gcc ctg ccc ggt gcg gcc ggc gcc ctg ccg ggt gcg      1081
105 Gly Ala Ala Gly Ala Leu Pro Gly Ala Ala Gly Ala Leu Pro Gly Ala
106          305          310          315
108 gcg ggc gcc gcg ggt gcg ttg ccg gcg gcc gcc ggc gcc gcg ccg gca      1129
109 Ala Gly Ala Ala Gly Ala Leu Pro Ala Ala Ala Gly Ala Ala Pro Ala
110          320          325          330
112 ctg ccc ccg gtc tag accttttcca aaccatccac cagacggcac c      1175
113 Leu Pro Pro Val
114          335
117 <210> SEQ ID NO: 2
118 <211> LENGTH: 336
119 <212> TYPE: PRT
120 <213> ORGANISM: mycobacterium avium paratuberculosis
122 <400> SEQUENCE: 2
124 Val Pro Asn Arg Arg Arg Arg Lys Leu Ser Thr Ala Met Ser Ala Val
125 1          5          10          15
128 Ala Ala Leu Ala Val Ala Ser Pro Cys Ala Tyr Phe Leu Val Tyr Glu
129          20          25          30

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132 Ser Thr Ala Gly Asn Lys Ala Pro Glu His His Glu Phe Lys Gln Ala
133      35      40      45
136 Ala Val Met Ser Asp Leu Pro Gly Glu Leu Met Gly Ala Leu Ser Gln
137      50      55      60
140 Gly Leu Ser Gln Phe Gly Ile Asn Leu Pro Pro Val Pro Ala Leu Ser
141 65      70      75      80
144 Gly Gly Ala Thr Ser Thr Pro Gly Leu Ala Ser Pro Gly Leu Gly Ser
145      85      90      95
148 Pro Gly Leu Gly Thr Pro Gly Leu Gly Thr Pro Gly Leu Thr Asn Pro
149      100     105     110
152 Gly Leu Thr Ser Pro Gly Ala Thr Ser Pro Gly Leu Thr Ser Pro Gly
153      115     120     125
156 Leu Thr Ser Pro Gly Leu Thr Ser Pro Gly Leu Thr Ser Pro Gly Ala
157      130     135     140
160 Ala Pro Thr Thr Pro Gly Leu Thr Ala Pro Gly Ala Leu Pro Thr Thr
161 145     150     155     160
164 Pro Gly Gly Gly Val Ala Thr Pro Gly Ala Gly Leu Asn Pro Ala Leu
165      165     170     175
168 Ser Asn Pro Gly Leu Thr Ser Pro Ala Gly Thr Ala Pro Gly Leu Gly
169      180     185     190
172 Ser Pro Thr Val Ala Pro Ser Glu Val Pro Ile Asp Ser Gly Ala Gly
173      195     200     205
176 Leu Asp Pro Gly Ala Gly Gly Thr Tyr Pro Ile Leu Gly Asp Pro Ser
177      210     215     220
180 Thr Phe Gly Asn Ala Ser Pro Ile Gly Gly Gly Thr Gly Leu Gly
181 225     230     235     240
184 Gly Gly Ser Ser Ser Gly Gly Ser Gly Gly Leu Val Asn Asp Val Met
185      245     250     255
188 Gln Ala Ala Asn Gln Leu Gly Ala Gly Gln Ala Ile Asp Leu Leu Lys
189      260     265     270
192 Gly Leu Val Met Pro Ala Ile Thr Gln Gly Met His Gly Gly Ala Ala
193      275     280     285
196 Ala Gly Ala Leu Pro Gly Ala Ala Gly Ala Leu Pro Gly Ala Ala Gly
197      290     295     300
200 Ala Leu Pro Gly Ala Ala Gly Ala Leu Pro Gly Ala Ala Gly Ala Ala
201 305     310     315     320
204 Gly Ala Leu Pro Ala Ala Ala Gly Ala Ala Pro Ala Leu Pro Pro Val
205      325     330     335
208 <210> SEQ ID NO: 3
209 <211> LENGTH: 600
210 <212> TYPE: DNA
211 <213> ORGANISM: mycobacterium avium paratuberculosis
214 <220> FEATURE:
215 <221> NAME/KEY: CDS
216 <222> LOCATION: (67)..(567)
218 <400> SEQUENCE: 3
219 ttcgagaagg gatagcaggc ggggcccggc ggtgaaccgc ggaggcgcgc ggtgcgtctt      60
221 cagggc atg tcc cgt ttg tca ttt gtc tgc agg ctt ttg gcc gca acc      108
222 Met Ser Arg Leu Ser Phe Val Cys Arg Leu Leu Ala Ala Thr

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223      1      5      10
225 gct ttc gcc gtc gcc ctg cta ctc ggg ctg ggc gac gtg ccg cgc gcg      156
226 Ala Phe Ala Val Ala Leu Leu Leu Gly Leu Gly Asp Val Pro Arg Ala
227 15      20      25      30
229 gcg gcc acc gac gac cgc ctg caa ttc acc gcg acc acg ctc agc ggc      204
230 Ala Ala Thr Asp Asp Arg Leu Gln Phe Thr Ala Thr Thr Leu Ser Gly
231      35      40      45
233 gcg ccg ttc aac ggc gcc agt ctg cag ggc aag ccc gcc gtg ctg tgg      252
234 Ala Pro Phe Asn Gly Ala Ser Leu Gln Gly Lys Pro Ala Val Leu Trp
235      50      55      60
237 ttc tgg acg ccg tgg tgc ccg tac tgc aac gcc gag gcc ccg ggc gtg      300
238 Phe Trp Thr Pro Trp Cys Pro Tyr Cys Asn Ala Glu Ala Pro Gly Val
239      65      70      75
241 agc cgg gtg gcc gcc gcc aac ccg ggc gtc acc ttc gtc ggc gtc gcc      348
242 Ser Arg Val Ala Ala Ala Asn Pro Gly Val Thr Phe Val Gly Val Ala
243      80      85      90
245 gcc cac tcc gaa gtc ggc gcc atg gcc aac ttc gtc tcc aag tac aac      396
246 Ala His Ser Glu Val Gly Ala Met Ala Asn Phe Val Ser Lys Tyr Asn
247 95      100      105      110
249 ctg aac ttc acc acg ctc aac gac gcc gac ggc gcg atc tgg gcc cgc      444
250 Leu Asn Phe Thr Thr Leu Asn Asp Ala Asp Gly Ala Ile Trp Ala Arg
251      115      120      125
253 tac ggc gtg ccc tgg cag ccc gcg tac gtg ttc tac ccg gcg gac ggc      492
254 Tyr Gly Val Pro Trp Gln Pro Ala Tyr Val Phe Tyr Arg Ala Asp Gly
255      130      135      140
257 agc tcc acc ttc gtc aac aac ccc acc tcg gcg atg ccc cag gac gaa      540
258 Ser Ser Thr Phe Val Asn Asn Pro Thr Ser Ala Met Pro Gln Asp Glu
259      145      150      155
261 ctg gcc gcc cgg gtg gcg gcg ctg cgc tgacgtggac cgcggtctgg      587
262 Leu Ala Ala Arg Val Ala Ala Leu Arg
263      160      165
265 tcgggctggc ggt      600
268 <210> SEQ ID NO: 4
269 <211> LENGTH: 167
270 <212> TYPE: PRT
271 <213> ORGANISM: mycobacterium avium paratuberculosis
273 <400> SEQUENCE: 4
275 Met Ser Arg Leu Ser Phe Val Cys Arg Leu Leu Ala Ala Thr Ala Phe
276 1      5      10      15
279 Ala Val Ala Leu Leu Gly Leu Gly Asp Val Pro Arg Ala Ala Ala
280      20      25      30
283 Thr Asp Asp Arg Leu Gln Phe Thr Ala Thr Thr Leu Ser Gly Ala Pro
284      35      40      45
287 Phe Asn Gly Ala Ser Leu Gln Gly Lys Pro Ala Val Leu Trp Phe Trp
288      50      55      60
291 Thr Pro Trp Cys Pro Tyr Cys Asn Ala Glu Ala Pro Gly Val Ser Arg
292 65      70      75      80
295 Val Ala Ala Ala Asn Pro Gly Val Thr Phe Val Gly Val Ala Ala His
296      85      90      95

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299 Ser Glu Val Gly Ala Met Ala Asn Phe Val Ser Lys Tyr Asn Leu Asn
300      100      105      110
303 Phe Thr Thr Leu Asn Asp Ala Asp Gly Ala Ile Trp Ala Arg Tyr Gly
304      115      120      125
307 Val Pro Trp Gln Pro Ala Tyr Val Phe Tyr Arg Ala Asp Gly Ser Ser
308      130      135      140
311 Thr Phe Val Asn Asn Pro Thr Ser Ala Met Pro Gln Asp Glu Leu Ala
312 145      150      155      160
315 Ala Arg Val Ala Ala Leu Arg
316      165
319 <210> SEQ ID NO: 5
320 <211> LENGTH: 366
321 <212> TYPE: DNA
322 <213> ORGANISM: mycobacterium avium paratuberculosis
325 <220> FEATURE:
326 <221> NAME/KEY: CDS
327 <222> LOCATION: (34)..(366)
329 <400> SEQUENCE: 5
330 tagcgggtgca ttgactgggg aaggtgtcca cac atg agg ctg tcg ttg agc aaa      54
331      Met Arg Leu Ser Leu Ser Lys
332      1      5
334 ttg ggc gtt gcg gtg ggc agc gcg gca gtg gca ttg acc gcc gcg gcc      102
335 Leu Gly Val Ala Val Gly Ser Ala Ala Val Ala Leu Thr Ala Ala Ala
336      10      15      20
338 ggt gtc gca tcc gcc gac ccc atg gac gcg atc atc aac acc acc tgc      150
339 Gly Val Ala Ser Ala Asp Pro Met Asp Ala Ile Ile Asn Thr Thr Cys
340      25      30      35
342 aac tac ggg cag gtg atc gcc gcg ctg aac gcg tcc gac ccg gcg gct      198
343 Asn Tyr Gly Gln Val Ile Ala Ala Leu Asn Ala Ser Asp Pro Ala Ala
344 40      45      50      55
346 gcc cag cag ctg aac tcg tcg ccg atg gcg cag tcc tac atc cag cgg      246
347 Ala Gln Gln Leu Asn Ser Ser Pro Met Ala Gln Ser Tyr Ile Gln Arg
348      60      65      70
350 ttc ctg gcc tcc ccg ccg gcg aag cgt cag cag atg gcc cag cag atc      294
351 Phe Leu Ala Ser Pro Pro Ala Lys Arg Gln Gln Met Ala Gln Gln Ile
352      75      80      85
354 cag ggc atg ccg gcc gcg cag cag tac atc aac gac atc aac cag gtc      342
355 Gln Gly Met Pro Ala Ala Gln Gln Tyr Ile Asn Asp Ile Asn Gln Val
356      90      95      100
358 gcg gtc acc tgt aac aac ttc tga      366
359 Ala Val Thr Cys Asn Asn Phe
360      105      110
363 <210> SEQ ID NO: 6
364 <211> LENGTH: 110
365 <212> TYPE: PRT
366 <213> ORGANISM: mycobacterium avium paratuberculosis
368 <400> SEQUENCE: 6
370 Met Arg Leu Ser Leu Ser Lys Leu Gly Val Ala Val Gly Ser Ala Ala
371 1      5      10      15

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/501,127A

DATE: 04/13/2005
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Input Set : A:\Sequence 2002-032 US.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 592,619
Seq#:9; Xaa Pos. 95,118,147
Seq#:10; Xaa Pos. 95,118,147
Seq#:15; N Pos. 331,398
Seq#:15; Xaa Pos. 103,125
Seq#:16; Xaa Pos. 103,125
Seq#:17; Xaa Pos. 88,99
Seq#:18; Xaa Pos. 88,99

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:466
M:341 Repeated in SeqNo=9
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:80
M:341 Repeated in SeqNo=10
L:930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:291
M:341 Repeated in SeqNo=15
L:984 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:96
M:341 Repeated in SeqNo=16
L:1034 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:17
L:1034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:392
L:1075 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:80
M:341 Repeated in SeqNo=18